

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/938,035A

Source:

OIP

Date Processed by STIC:

5-23-02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

# Does Not Comply Raw Sequence Listing Error Summary Corrected Diskette Needed

## ERROR DETECTED

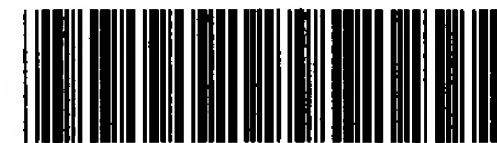
## SUGGESTED CORRECTION

SERIAL NUMBER: 09/938,035A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length    The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII    The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      Variable Length    Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"    A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)    Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
                    (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                    (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                    This sequence is intentionally skipped  
  
                    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)    Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
                    <210> sequence id number  
                    <400> sequence id number  
                    000
- 9      Use of n's or Xaa's  
    (NEW RULES)    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                    Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      Invalid <213>  
    Response    Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>    Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
                    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                    (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"    Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

Does Not Comply  
Corrected Diskette Needed



OIPE

## RAW SEQUENCE LISTING

DATE: 05/23/2002

PATENT APPLICATION: US/09/938,035A

TIME: 18:06:05

Input Set : A:\seq list-20731,RocheVit.txt

Output Set: N:\CRF3\05232002\I938035A.raw

3 <110> APPLICANT: Roche Vitamins AG  
 5 <120> TITLE OF INVENTION: Microbial process for producing L-ascorbic acid and  
 6 D-erythorbic acid  
 8 <130> FILE REFERENCE: Alicyclobacillus NA20, 21, FJ21 16S nuc  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/938,035A  
 C--> 11 <141> CURRENT FILING DATE: 2001-08-23  
 13 <150> PRIOR APPLICATION NUMBER: EP Application No. 00118059.5  
 14 <151> PRIOR FILING DATE: 2000-08-23  
 16 <160> NUMBER OF SEQ ID NOS: 3  
 18 <170> SOFTWARE: PatentIn Ver. 2.1

## ERRORED SEQUENCES

98 <210> SEQ ID NO: 3  
 99 <211> LENGTH: 1495  
 100 <212> TYPE: DNA  
 101 <213> ORGANISM: Alicyclobacillus sp.  
 103 <220> FEATURE:  
 104 <221> NAME/KEY: rRNA  
 105 <222> LOCATION: (1)..(1495)  
 106 <223> OTHER INFORMATION: FJ-21 Partial 16SrRNA gene sequence  
 108 <400> SEQUENCE: 3  
 109 aggacgaacg ctggcggcgt gcctaataca tgcaagtcca gcggacctct tctgaggtca 60  
 110 gcggcggaac ggtgaggaac acgtgggtaa tctgcctttc agaccggaat aacgcccgga 120  
 111 aacgggcgct aatgccgat acgcccgcga ggaggcatct tcttgccggg aaaggcccga 180  
 W--> 112 ttgggcccgt gagagaggag cccgcggcgc attagcctgt tggcggggta acggcccacc 240  
 113 aaggcgacga tgcgtagccg acctgagagg gtgaccggcc acactgggac tgagacacgg 300  
 114 cccagactcc tacgggaggg agcagtaggg aatcttcgcg aatgggcgca agcctgacgg 360  
 115 agcaacgccg cgtgagcgaa gaaggccttc gggttgtaaa gctctgttgc tcggggagag 420  
 116 cggcatgggg agtggaagc cccatgcgag acggtaccca gtgaggaagc cccggctaac 480  
 117 tacgtgccag cagccgcggt aaaacgtagg gggcgagcgt tgtccggaat cactgggcgt 540  
 118 aaaggggtgc taggcggtcg agcaagtctg gagtgaaggt ccatggctca accatgggat 600  
 119 ggctctggaa actgcttgac ttgagtgtcg gagaggcaag gggaattcca cgtgtagcgg 660  
 120 tgaaatgcgt agagatgtgg aggaatacca gtggcggaag cgccttgctg gacagtgact 720  
 121 gacgctgagg cacgaaagcg tggggagcaa acaggattag ataccctggt agtccacgcc 780  
 122 gtaaacgatg agtgctaggt gttgggggga cacaccccag tgccgaagga aacccaataa 840  
 123 gcaactccgc tggggagtac ggtcgcaaga ctgaaactca aaggaattga cgggggcccc 900  
 124 cacaagcagt ggagcatgtg gtttaattcg aagcaacgcg aagaacctta ccagggcttg 960  
 125 acatccctct gacgggtgca gagatgcacc ttcccttcgg ggcagaggag acaggtgggt 1020  
 126 catggttgct gtcagctcgt gtcctgagat gttgggttca gtcccgaac gagcgcaacc 1080  
 W--> 127 cttgacctgt gttaccagcg cgttggggc gggactcaca ggtgactgcc ggcgtaagtc 1140  
 128 ggaggaaggg ggggatgacg tcaaatacat atgcccctga tgtcctgggc tacacacgtg 1200

see item # 9  
on ERROR SUMMARY  
SHEET

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/938,035A

DATE: 05/23/2002

TIME: 18:06:05

Input Set : A:\seq list-20731,RocheVit.txt

Output Set: N:\CRF3\05232002\I938035A.raw

129 ctacaatggg cggtagaaag ggagggcgaag ccgcgaggcg gaggcgaacc caaaaagccg 1260  
130 ctgtagttc ggattgcagg ctgcaactcg cctgcatgaa gccggaattg ctagtaatcg 1320  
131 cggatcagca tgccgcggtg aatacgttcc cgggccttgt acacaccgcc cgtcacacca 1380  
132 cgagagtcgg caacaccgga agtcggtgag gtaaccccgga aaggggagcc agccgccgaa 1440  
133 ggtgggggtcg atgattgggg tgaagtcgta acaaggtagc cgtaccggaa ggtgc 1495

E--&gt; 136 1

E--&gt; 139 1

Remove extra material at end  
of file

## VERIFICATION SUMMARY

DATE: 05/23/2002

PATENT APPLICATION: US/09/938,035A

TIME: 18:06:06

Input Set : A:\seq list-20731,RocheVit.txt

Output Set: N:\CRF3\05232002\I938035A.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:34 M:341 W (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:180  
L:47 M:341 W (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:960  
L:54 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1380  
L:73 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:180  
L:112 M:341 W (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:180  
L:127 M:341 W (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:1080  
L:136 M:254 E No. of Bases conflict, this line has no nucleotides.  
M:254 Repeated in SeqNo=3